

0570  
10/2

OIEP

#2

## RAW SEQUENCE LISTING

DATE: 12/06/2001

PATENT APPLICATION: US/09/924,231

TIME: 12:20:19

Input Set : N:\Crf3\RULE60\09924231.txt

Output Set: N:\CRF3\12062001\I924231.raw

5 <110> APPLICANT: SPEAR, Patricia G.  
 7 MONTGOMERY, Rebecca I.  
 11 <120> TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN  
 15 <130> FILE REFERENCE: 0290-1  
 19 <140> CURRENT APPLICATION NUMBER: 09/924,231  
 21 <141> CURRENT FILING DATE: 2001-08-08  
 23 <150> PRIOR APPLICATION NUMBER: 09/333,279  
 25 <151> PRIOR FILING DATE: 1999-06-15  
 29 <160> NUMBER OF SEQ ID NOS: 7  
 33 <170> SOFTWARE: PatentIn Ver. 2.0  
 37 <210> SEQ ID NO: 1  
 39 <211> LENGTH: 1724  
 41 <212> TYPE: DNA  
 43 <213> ORGANISM: Homo sapiens  
 47 <400> SEQUENCE: 1

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 53 cccctgctg cccactctcc tgctgtcggg gttctgaggg acagcttgct acaccgaggg 180  
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 59 ctccctggaga ctgggggcct cctccctgga gatccacccc cagaaccgac gtcttgaggg 360  
 61 tgggtgctgta tctcaccttc ctgggagccc cctgtctacgc cccagctctg ccgtcctgca 420  
 63 aggaggacga gtacccagtg ggctccgagt gctgccccaa gtgcagtcca gggtatctgt 480  
 65 tgaaggaggc ctgcggggag ctgacgggca cagtgtgtga accctgccct ccaggcacct 540  
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 73 cctccagccc gggccagagg gtgcagaagg gaggcaccga gagtcaggac accctgtgtc 780  
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 85 acgtcaccac ggtggccgtg gaggagacaa taccctcatt cacggggagg agcccaaacc 1140  
 87 actgaccac agactctgca ccccgacgcc agagatacct ggagcgacgg ctgctgaaag 1200  
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 103 ggtcctgtct tctatttgtc atgaaacagt gtatttgggg agatgctgtg ggaggatgta 1680  
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 109 <210> SEQ ID NO: 2  
 111 <211> LENGTH: 283  
 113 <212> TYPE: PRT

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133 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
135           35           40           45
139 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
141           50           55           60
145 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
147   65           70           75           80
151 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
153           85           90           95
157 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
159           100          105          110
163 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
165           115          120          125
169 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
171           130          135          140
175 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
177 145          150          155          160
181 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
183           165          170          175
187 Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
189           180          185          190
193 Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
195           195          200          205
199 Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
201           210          215          220
205 Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
207 225          230          235          240
211 Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu
213           245          250          255
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247 <210> SEQ ID NO: 4
249 <211> LENGTH: 22
251 <212> TYPE: DNA
253 <213> ORGANISM: Homo sapiens
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281 <211> LENGTH: 4622
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295 gtcttgaggc tgggtgctgta tctcaccttc ctgggagccc cctgctacgc cccagctctg 180
297 ccgtcctgca aggaggacga gtacccagtg ggctccgagt gctgccccaa gtgcagtcca 240
299 ggttatcgtg tgaaggaggc ctgcggggag ctgacgggca cagtgtgtga accctgccct 300
301 ccaggcacct acattgccc cctcaatggc ctaagcaagt gtctgcagtg ccaaattgtg 360
303 gaccagcca tgggcctgcg cgcgagccgg aactgctcca ggacagagaa cgccgtgtgt 420
305 ggctgcagcc caggccactt ctgcatcgtc caggacgggg accactgctc cgctgcccgc 480
307 gcttacgcca cctccagccc gggccagagg gtgcagaagg gaggcaccga gagtccaggc 540
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369 cgtaagggga ttttgggtcat gagattatca aaaaggatct tcacctagat ctttttaaat 2400
371 taaaaatgaa gttttaaatc aatctaaaagt atatatgagt aaacttggtc tgacagttac 2460
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453 &lt;212&gt; TYPE: PRT

455 &lt;213&gt; ORGANISM: Homo sapiens

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467 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala

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485 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
487 65          70          75          80
491 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
493          85          90          95
497 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
499          100          105          110
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553          245          250          255
557 Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile
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563 Arg Val Val Ser Thr Leu Pro Ile Thr His Gln Asp Trp Leu Arg Gly
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577 305          310          315          320
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583          325          330          335
587 Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu
589          340          345          350
593 Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Ala
595          355          360          365
599 Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Asn Lys Leu Ser Val
601          370          375          380
605 Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met
607 385          390          395          400
611 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Arg Ser
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